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Database :
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Maximum Match 100%
Listing first 45 summaries

PIR_68:*
: pir1:*
: pir2:*
pir3.*
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pir1:*
pir2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ເນ	Score	% Query Match	Length	DВ		ription
; ; ;	176	. 1	115	ㅁ ;	PTHU	parathyroid hormon
2	168	95.5	115	L	PTPG	
ω	167		115	Ľ	PTBO	
4	167		115	2	JC4202	
5	158	•	115	N	A05091	parathyroid hormon
o	150		105	N	151851	
7	121		119	2	A34937	parathyroid hormon
8	61		824	N	F72408	leucinetRNA liga
9	58		175	Н	JN0103	parathyroid hormon
10	58		177	ب	PTHU2L	parathyroid hormon
11	58		177	سم	A30012	parathyroid hormon
12	58		177	2	JC4201	parathyroid hormon
13	58		209	 3	PTHU3L	parathyroid hormon
14	56		115	N	H72705	$\mathbf{-}$
15	55	•	94	N	T09450	virulence-associat
16	55		94	Ν	C64559	virulence associat
17	54	•	176	1	S10202	parathyroid hormon
18	54	•	564	Ν	T38291	GATA-type transcri
19	54	•	564	N	T43298	transcription fact
20	54	•	1257	Н	I58383	retinoblastoma bin
21	54	٠	2470	N	S57085	1-phosphatidylinos
22	52	•	363	N	F70195	UDP-N-acetylglucos
23	Ë		508		A43713	calcium-dependent
24		•	528	Ν	D65214	hypothetical 60.8
25	۲.	•	528	N	G86099	hypothetical prote
26	۳.		560	2	C41539	_
27	۲.		569	N	I53013	
		•	776			
28	51	•	330	N	F84056	hypothetical prote

A;Molecule type: protein
A;Residues: 32-68 <NIA>
A;Residues: 32-68 <NIA>
R;Brewer Jr., H.B.; Falrwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972
A;Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residue
A;Reference number: A93783; MUID:73070429
A;Accession: A93783

A; Molecule type: protein

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
49.5	49.5	49.5	50	50	50	50	50	50	50.5	50.5	51	51	51	51	51
28.1	28.1	28.1	28.4	28.4	28.4	28.4	28.4	28.4	28.7	28.7	29.0	29.0	29.0	29.0	29.0
564	490	339	3678	2473	722	722	570	91	3394	145	2479	2182	1038	764	752
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HMIVC2	S71776	T18926	S28916	S38040	C72040	B86583	G72595	C64069	T18501	E84938	MNWVRA	T14320	T15098	ввни	C2HU
hemagglutinin prec	calcium-dependent	hypothetical prote	dystrophin - mouse	1-phosphatidylinos	transcription elon	transcription elon	hypothetical prote	virulence-associat	hypothetical prote	flagellar fliJ pro	nonstructural poly	calcineurin inhibi	hypothetical prote	complement factor	complement C2 prec

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Dec-2000; , A90426; y, G.N.;
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parathyroid hormone precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
C;Accession: B26806; A90390; A90376; A01535
R;Schmelzer, H.J; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid h
A;Reference number: A26806; MUID:87316938
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R;Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.; Potts Jr
Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979
A;Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid h
A;Reference number: A93835; MUID:80056617
A;Accession: A93835
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A; Residues: 32-109 <SAU>
R; Brown Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A; Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hor
A; Reference number: A90030; MUID:74173303
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A;Title: Isolation and complete nucleotide sequence of the gene for bovine parathyroi A;Reference number: A24949; MUID:84262483
A;Accession: A24949;
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A;Note: the authors translated the codon GAA for residue 50 as Gly
R;Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.; Cohn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identification, biosynthesis, and partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts
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R;Weaver, C;A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.
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F;32-115/Product: parathyroid hormone #status experimental <WAT>
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R; Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riord
Biochemistry 13, 1994-1999, 1974
A; Tile: The amino acid sequence of porcine parathyroid hormone.
A; Reference number: A90376; MUID:74253317
A; Accession: A90376
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1.9e-14;
thes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keywords: calcium; hormone; parathyroid gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Porcine proparathyroid hormone. 3, Reference number: A90390; MUID: 76018954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parathyroid hormone precursor - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: parathyroid hormone;
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A; Note: the authors translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Conservative
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Matches 31; Conserv
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A; Residues: 1-115 <SCH>
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A; Residues: 1-115 <WEA>
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              A: Residues: 32-52,'0',54-58,'K',60,'L',62-65 < CBRE>
A: Note: this sequence was determined by sequenator and mass spectroscopic identification R: Returnant, H-T: Niall, H-D: O'Riordan, J.L.H.: Potts Jr., J.T.
Biochemistry 14, 1842-1847, 1975
A: Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone. A: Accession: A90387; MUID:75146516
A: Accession: A90387; MUID:75146516
A: Molecule type: protein
A: Residues: 52-75 < KEE3>
A: Mill: Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 17, 5723-5729, 1978
A: Title: Complete amino acid sequence of human parathyroid hormone.
A: Reference number: A90426; MUID:79082855
A: Molecule type: protein
A: Residues: 61-106,'D', 108-115 < KEU>
A: Residues: 61-106,'D', 108-115 < KEU>
A: Retence number: A94410
A: Residues: 75-100 < KEE2>
A: Molecule type: protein
A: Accession: A94410
A: Accession: A94410
A: Accession: A94410
A: Molecule type: protein
A: Molecule type: protein
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A: Molecule type: Molecule
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A; Contents: annotation; synthesis of residues 32-65
A; Note: the biologically active amino-terminal 34 residues of parathyroid hormone were star renal adenylate cyclase assay and with the bovine hormone's active region in the chic R; Andreatta, R. H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel, Helv. Chim. Acta 56, 470-473, 1973
A; Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
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A; Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and phosphate; released
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Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
Pritle: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone. A;Reference number: 138342; MUID:82150870
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C:Superfamily: parathyroid hormone; parathyroid hormone homology
C:Keywords: calcium; hormone; parathyroid qland; plasma
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A,Description: factor in homeostatic control of plasma calcium
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Pred. No. 1.9e-15;
1; Mismatches 0;
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A;Gene: GDB:PTH A;Cross-references: GDB:119522; OMIM:168450

A; Map position: 11p15.2-11p15.1

A; Introns: 29/

A; Status: translated from GB/EMBL/DDBJ

R; Hendy, G.N.; MIL Proc. Natl. Acad.

A; Residues: 1-115 <RES> A; Molecule type: mRNA A; Accession: I38342

A; Reference number: A91635; MUID:73227467

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SYSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF

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RESULT PTPG

97.18;

Ouery Match 100. Best Local Similarity 97.1 Matches 33; Conservative

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Gaps

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R;Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A;Fitle: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid h
A;Reference number: A26806; MUID:87316938
                                                                                                                                                             canine parathyroid hormone-related protein a
                                                                                                 DeWille, J.W.; Capen,
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C;Species: Rattus norvegicus (Norway rat)
C;Acession-151851
R;Schmelzer, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Jul-1999
C;Accession: A05091; A26806
C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1995 #sequence_revision 27-oct-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                      A; Residues: 1-115 <RGS>
A; Cross-references: GB:U15662; NID:9558915; PIDN:AAA82584.1; PID:9558916
C; Superfamily: parathyroid hormone; parathyroid hormone homology
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A;Cross-references: GB:K01268; NID:g206483; PIDN:AAA41979.1; PID:g206485
A;Note: the authors translated the codon GAA for residue 87 as Asp
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Pred. No. 3.6e-13;
4; Mismatches 1; Indels
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J. Biol. Chem. 259, 3320-3329, 1984
A;Reference number: A05091; MUID:84135846
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                                                                                                 Steinmeyer, C.L.; McCauley, L.K.; Groene, A.;
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Pred. No. 2.6e-14;
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                                                         C;Accession: JC4202
R;Rosol, T.J.; Steinmeyer, C.L.; McCauley,
Gene 160, 241-243, 1995
A;Title: Sequences of the cDNAs encoding of
A;Reference number: JC4201; MUID:95369696
A;Accession: JC4202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parathyroid hormone precursor - rat
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Best Local Similarity 85.3%;
Matches 29; Conservative
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Best Local Similarity
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C; Superfamil:
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A;Molecule type: protein
R;Rseidues: 26-115 cHAM.
R;Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach, G.D.; Pott
Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970
A;Title: The amino acid sequence of bovine parathyroid hormone I.
A;Reference number: A91648; MUID:71076162
A;Accession: A91648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Mesidues: 32-115 CaRRE>
A; Residues: 32-115 CaRRE>
R; Potts Jr., Jr.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.;
Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
A; Title: Synthesis of a biologically active N-terminal tetratriacontapeptide of parathyr
A; Reference number: A93776; MUD:71091588
A; Reference number: A93776; MUD:71091588
A; Contents: annotation; synthesis of residues 32-65
A; Note: the synthetic peptide was active in vivo and in vitro
A; Neter Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
Am. J. Med. 56, 759-766, 1974
A; Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormon
A; Reference number: A90030; MUID:74173303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Weaver, C.A.; Gordon, D.F.
Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
A.Title: Introduction by molecular cloning of artifactual inverted sequences at the 5'
A.Reference number: 145975; WUID:82037785
A.Accession: 145975
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                A;Title: The N-terminal amino-acid sequence of bovine proparathyroid hormone. A;Reference number: A93793; MUID:74142666 A;Accession: A93793
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Mol. Cell. Endocrinol. 28, 411-424, 1982
A;Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA A;Reference number: 145976; MuID:83105964
A;Accession: 145976
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-115 <WE3>
A; Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645
C; Genetics:
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A;Introns: 29/2
C;Superfamily: parathyroid hormone; parathyroid hormone homology
C;Seywords: hormone
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-115/Product: proparathyroid hormone #status experimental <PMAT>F;26-31/Domain: propaptide #status experimental <PMAT>F;36-64/Domain: parathyroid hormone homology <PTH>
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                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 32-115 <NIA>
R; Brewer Jr., H.B.; Ronan, R.
Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970
A; Title: Bovine parathyroid hormone: amino acid sequence.
A; Reference number: A93773; MUID:71063634
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Pred. No. 2.6e-14;
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Sci. U.S.A. 71, 653-656, 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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91.2%;
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Best Local Similarity
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Gaps

Adv. Gene Technol. 21, 228-229, 1984

- dog

JC4202 parathyroid hormone precursor

Matches

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N;Alternate names: parathyroid hormone-like protein
N;Cohleans: parathyroid hormone-related protein, splice form 1; parathyroid hormone-related protein, splice form 1; parathyroid hormone-re;Species: Homo sapiens (ann)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: A33360; A28120; A94295; B94295; A36166; A91606; A28034; A36512;
B;Yasuda, T.: Banville, D.; Hendy, G.N.; Goltzman, D.
J. Biol. Chem. 264, 7720-7725, 1989
A;Title: Characterization of the human parathyroid hormone-like peptide gene. Functio A;Reference number: A33360; MUID:89214227
                                                                                                                                                                                   A;Cross-references: GB:AE001702; GB:AE000512; NID:94980662; PIDN:AAD35261.1; PID:9498
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A;Residues: 1-175 <YAS>
A;Cross-references: GB:M24349; GB:J04710; NID:g190708; PIDN:AAA60358.1; PID:g190712
A;Accession: B33360
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JN0103
C;Accession: JN0103
C;Accession: JN0103
C;Accession: JN0103
C;Accession: JN0103
A;Reite: Structure of the mouse gene encoding parathyroid hormone-related peptide.
A;Reference number: JN0103; MUID:91065532
A;Reference number: JN0103
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C;Comment: The normal role of the parathyroid hormone-related peptide is unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 34/2; 173/2
C; Superfamily: parathyroid hormone-related protein; parathyroid hormone homology
F;1-24/Domain: signal sequence #status predicted <SIG>
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F;35-69/Domain: parathyroid hormone homology <PTH>
F;37-175/Product: parathyroid hormone-related peptide #status predicted <MAT>
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                                                                                                                                                                                                                                                                                            A;Gene: TM0168
C;Superfamily: leucine--tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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6.2;
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Pred. No. 2.9;
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Pred. No.
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692 MELVNHLSQYLNSVPQEEWNRKLLREI 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.7%;
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34.4%;
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Best Local Similarity 37.0%
Matches 10; Conservative
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A; Residues: 176-177 <YAS2>
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Best Local Similarity
                                                                                                A; Molecule type: DNA
A; Residues: 1-824 <ARN>
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                                                              A;Status: preliminary
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                    A; Accession: F72408
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72408
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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Nature 399, 323-329, 1999
A;Fitle: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316
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A;Title: Nucleotide sequence of cloned cDNas encoding chicken preproparathyroid hormone. A;Reference number: 150411; MUID:89284968
        Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
nce number: 151851
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A;Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyrc A;Reference number: 151851
A;Reference number: 151851
A;Accession: 15185
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A; Cross-references: GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g212592
A; Cross-references: GB:M36522; NID:g212591; PIDN:AAB02866.1; PID:g212592
C; Superfamily: parathyroid hormone; parathyroid hormone homology
F; 1-25/Domain: propeptide #status predicted <PRO>
F; 36-4/Domain: parathyroid hormone homology <PTH>
F; 32-119/Product: parathyroid hormone #status predicted <MAT>
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C;Superfamily: parathyroid hormone; parathyroid hormone homology
F;20-54/Domain: parathyroid hormone homology <PTH>
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Pred. No. 3.4e-12;
5; Mismatches 2; Indels
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Pred. No. 1.9e-08;
9; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: 150411
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 AISEIQLMHNLGKHLASVERMQWLRKKLQDGHNF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.2%;
7.9.4%;
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Best Local Similarity 63.6%;
Matches 21; Conservative
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Best Local Similarity 79.4
Matches 27; Conservative
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PID:9200566

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Banville,

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A.Molecule type: DNA
A.Residues: 1-177 < KARN
A.Residues: 1-177 < KARN
A.Cross-references: GB.M34112; NID:9206229; PIDN:AAA41889.1; PID:9206231
A.Note: the authors translated the codon TAC for residue 114 as Thr
R.Yasuda, T.; Banville, D.; Rabbani, S.A.; Hendy, G.N.; Goltzman, D.
Mol. Endocrinol. 3, 518-525, 1989
A.Title: Rat parathyroid hormone-like peptide: comparison with the human homologue an A.Reference number: A34944; MUID:89313794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Soifer, N.E.; Dee, K.E.; Insogna, K.L.; Burtis, W.J.; Matovcik, L.M.; Wu, T.L.; Mil J. Biol. Chem. 267, 18236-18243, 1992
A;Title: Parathyroid hormone-related protein. Evidence for secretion of a novel mid-r A;Reference number: A43416; MUID:92388199
A;Accession: A43416
                                                                                                                      A; Title: Gene-encoding parathyroid hormone-like peptide: nucleotide sequence of the A; Reference number: A34723; WUID:90258937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-177 <THI>
A;Cross-references: EMBL:M21967; NID:g206488; PIDN:AAA41981.1; PID:g206489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A;Residues: 'X',75-84,'S',86-90,'X',92-93,'X',95-101,'X',103-105,'X',107
A;Experimental source: RIN-141 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-177 <YAS>
A;Cross-references: GB:M31603; NID:9206486; PIDN:AAA41980.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: sequence extracted from NCBI backbone (NCBIP:112971)
                                        R;Karaplis, A.C.; Yasuda, T.; Hendy, G.N.; Goltzman, Mol. Endocrinol. 4, 441-446, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Expression of a calcium-mobilizing A;Reference number: A30012; MUID:89019361
    C; Accession: A34723; A34944; A30012; A43416
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34.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Thiede, M.A.; Rodan, G.A.
Science 242, 278-280, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                        A; Accession: A34723
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A; Residues: 37-70, 'x', 72-84, 'x', 86;103-115 <SUV2>
R; Thiede, M.A.; Strewler, G.J.; Nissenson, R.A.; Rosenblatt, M.; Rodan, G.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 4609, 1988
A; Title: Human renal carcinoma expresses two messages encoding a parathyroid hormone-lik
A; Reference number: A36166; MUID:88262996
A; Accession: A36166.
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R;Moseley, J.M.; Kubota, M.; Diefenbach-Jagger, H.; Wettenhall, R.E.H.; Kemp, B.E.; Suva Proc. Natl. Acad. Sci. U.S.A. 84, 5048-5052, 1987
A;Title: Parathyroid hormone-related protein purified from a human lung cancer cell line A;Reference number: A28034; MUID:87260926
                                    R;Mangin, M.; Webb, A.C.; Dreyer, B.E.; Posillico, J.T.; Ikeda, K.; Weir, E.C.; Stewart, Proc. Natl. Acad. Sci. US.A. 85, 597-601, 1988
A;Title: Identification of a cDNA encoding a parathyroid hormone-like peptide from a hum A;Reference number: A28120; MUID:88124888
                                                                                                                                                                                                                                                                                                                                                   R;Suva, L.J.; Winslow, G.A.; Wettenhall, R.E.H.; Hammonds, R.G.; Moseley, J.M.; Diefenba
Science 237, 893-896, 1987
A;Title: A parathyroid hormone-related protein implicated in malignant hypercalcemia; cl
A;Reference number: A94295; MUID:87292119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-175 c7H1.
A; Cross-references: GB:J03802; NID:g190717; PIDN:AAA60218.1; PID:g190718
R; Suva, L.J.; Mather, K.A.; Gillespie, M.T.; Webb, G.C.; Ng, K.W.; Winslow, G.A.; Wood, Gene 77, 95-105, 1989
A; Title: Structure of the 5' flanking region of the gene encoding human parathyroid-horn A; Reference number: A91606; MUID:89306685
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A;Residues: 37-52 <MOS>
C;Comment: This hormone stimulates an increase of cyclic AMP levels in osteoblasts and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;25-36/Domain: propeptide #status predicted <PRO>F;35-69/Domain: parathyroid hormone homology <PTH>>F;37-69/Domain: parathyroid hormone-rolated peptide, splice form 2 #status predicted F;37-177/Product: parathyroid hormone-rolated peptide, splice form 1 #status predicted F;37-175/Product: parathyroid hormone-related peptide, splice form 1 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ay a role in fetal calcium metabolism.

C;Genetics:
A;Gene: GDB:PTHLH
A;Cross-references: GDB:120323; OMIM:168470
A;Map position: 12p12.1-12p11.2
A;Introns: 34/2
C;Superfamily: parathyroid hormone-related protein; parathyroid hormone homology C;Keywords: alternative splicing; hormone; humoral hypercalcemia
F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:M17183; NID:q190725; PIDN:AAA60221.1; PID:q190726
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Pred. No. 2.9;
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34.4%;
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A; Cross-references: GB:J04710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-177 <SUV1>
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A; Residues: 1-34 <SUV3>
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Best Local S
Matches 11
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parathyroid hormone-like peptide in lacta

PID:9206487

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canine parathyroid hormone-related protein a
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C;Species: Canis lupus familiaris (dog)
C;Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 16-Jul-1999
C;Accession: JG4201
R;Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, Gene 160, 241-243, 1995
A;Fitle: Sequences of the cDNAs encoding canine parathyroid hormone-related protein A;Reference number: JG4201; MUID:95369696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U15593; NID:g558476; PIDN:AAA82583.1; PID:g558477 C;Superfamily: parathyroid hormone-related protein; parathyroid hormone homology
        hormone homology
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C; Superfamily: parathyroid hormone-related protein; parathyroid hormone homolc F;1.36/Domain: signal sequence #status predicted <SIG>F;1.56/Domain: parathyroid hormone homology <PTHS>F;35-69/Domain: parathyroid hormone-luke protein #status predicted <AMAT>F;37-117/Product: parathyroid hormone-like protein #status predicted <AMAT>F;37-74/Cleavage site: Arg-Ala (unidentified proteinase) #status experimental
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F:37-177/Product: parathyroid hormone related protein #status predicted <MAT>
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Pred. No. 2.9;
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AVSEHOLLHDKGKSIODLRRRFFLHHLIAEIH 68
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A; Residues: 1-177 <ROS>
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A30012
parathyroid hormone-like protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

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Gaps

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Indels

12;

9; Mismatches

1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32 :||| ||:|: || : : | :| : : ::|
37 AVSEHQLLHDKGKSIQDLRRRFFLHHLIAEIH ö

Pred. No. 2.9; 9; Mismatches

Best Local Similarity 34.4%; Matches 11; Conservative

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C; Species: Helicobacter pylori
C; Date: 16-Uii-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession: T09450
R; Cao, P.; Cover, T.L.
A; Bacteriol. 179, 2852-2856, 1997
A; Title: High-level genetic diversity in the vapD chromosomal region of Helicobacter A; Reference number: 216675; MUD: 97284485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: U94318; NID: 92072451; PIDN: AAC45241.1; PID: 92072452
                                                                                                                                     Gaps
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                                            Length 115;
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Pred. No. 3.6;
                                                DB 2;
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                                                                                3.4;
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C;Superfamily: virulence-associated protein vapD
C;Keywords: virulence
                                                                                                                                     Mismatches
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                                            Score 56;
Pred. No.
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Job time: 49 sec
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17 EVAALYILHRLGPTLNYGEAVEILRERL
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                                        31.8%;
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31.8%;
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Matches 7; Conservative
                                                                                                                                 Conservative
                                                Query Match
Best Local Similarity
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A; Residues: 1-94 <CAO>
                                                                                                                                     12;
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A;Residues: 176-209 <MAN>
A;Cross-references: GB:M34071; NID:g190715; PIDN:AAA60217.1; PID:g190716
C;Comment: This hormone causes humoral hypercalcemia of malignancy when secreted by cert
                                                                                                                                                                                                                                                                                    PRESULT 13
PTHU3L
parathyroid hormone-related protein precursor, splice form 3 - human
N:Alternate names: parathyroid hormone-like protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 2314Mar. 1993 #sequence_revision 31-Mar-1993 #text_change 18-Jun-1999
C;Accession: C33360; A3276
R;Yasuda, T.; Banville, D.; Hendy, G.N.; Goltzman, D.
J; Biol. Chem. 264, 7720-7725, 1989
A;Title: Characterization of the human parathyroid hormone-like peptide gene. Functional
A;Reference number: A33360; MUID:89214227
A;Accession: C33360
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A; Cross.
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: parathyroid hormone-related protein; parathyroid hormone homology C;Reywords: alternative splicing; hormone; humoral hypercalcemia
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    Gaps
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    Indels
12;
                                                                                    1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32
                                                                                                                                     A;Cross-references: GDB:120323; OMIM:168470
A;Map position: 12p12.1-12p11.2
A;Introns: 34/2; 175/2
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hypothetical protein APE1063 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72705
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kawa. H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kaya. H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kaya. H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kaya. H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kaya. H.; Takamiya, M.; Masuda, M.; Masuda,

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Gaps

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Score 58; DB 1; Length 209; Pred. No. 3.5; 9; Mismatches 12; Indels

33.0%; 34.4%;

Query Match 33.0 Best Local Similarity 34.4 Matches 11; Conservative

C; Genetics:

1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32

:||| ||:|: || : : | :| 37 AVSEHQLLHDKGKSIQDLRRRFFLHHLIAEIH

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14

A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA80048.1; PID:d1043834; PID:g510 A;Experimental source: strain Kl C;Genetics:

A; Molecule type: DNA A; Residues: 1-115 <KAW> A; Status: preliminary

A; Gene: APE1063

us-09-447-800-1.rpr

ca e e ha ta i c

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August 8, 2001, 16:29:17 ; Search time 10.12 Seconds (without alignments) 115.088 Million cell updates/sec
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sus scrofa
bos taurus
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
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                                                                                                                                        93435 segs, 34255486 residues
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PTHY_CHICK
SYL_THEMA
PTHR_MOUSE
PTHR_CANFA
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PTHR_RAT
VAPD_HELPY
PTHR_CHICK
GAF2_SCHPO
RBB1_HUMAN
TOR1_YEAST
MURG_BORBU
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PTH_MACFA
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PTHY_CANFA
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Listing first 45 summaries
                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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homo sapien homo sapien rattus norv

KNLC_RAT KNLC_HUMAN HBS1_YEAST CO2_HUMAN CFAB_HUMAN

ECOLI CDPK_SOYBN

buchnera ap riemerella

POLN_RRVN FLIJ_BUCAI VAP1_RIEAN

CABI_RAT

ross river

haemophilus chlamydia p

saccharomyc mus musculu

Q9z7g4 P32600 P11531 P71351

GREA_CHLPN TOR2_YEAST DMD_MOUSE

glycine max escherichia rattus norv homo sapien saccharomyc 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDITINE-9129748; PubMed=2069952; Rlaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.; Rlaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.; Investigation of the solution structure of the human parathyroid hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry, and molecular dynamics calculations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "JY-CLIN. INVEST. 86:1084-1087(1990).
-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
-!- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.; "Solution structures of human parathyroid hormone fragments Phyth(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
                                                                                                                                                                          MEDLINE=75059220; PubMed=4474131; Tregear G.W., van Rietschoten J., Green E., Niall H.D., Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.; Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human parathyroid hormone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 32-68.
MEDLINE-95318084; PubMed-7797503;
Marx U.C., Austermann S., Bayer P., Adermann K., Ejchart A.,
Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJINE=93345518; PubMed-8344299;
Barden J.A., Cuthbertson R.M.;
"Stabilized NMR structure of human parathyroid hormone(1-34).";
Eur. J. Biochem. 215:315-321(1993).
                                                            Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
A reinvestigation of the amino-terminal sequence of human
                                                                                                                                                                                                                                                                                                                                        MEDLINE-73227467; PubMed-4721748; Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R., Riniker B., Rittell W., Sieber P.; "Synthesis of sequence 1-34 of human parathyroid hormone."; Hely. Chim. Acta 56:470-473(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of human parathyroid hormone 1-37 in solution."; J. Biol. Chem. 270:15194-15202(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91009811; PubMed-2212001;
Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOPARATHYROIDISM (FIH). SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 267:213-220(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20090619; PubMed=10623601;
                                     MEDLINE=75146516; PubMed=1125201;
                                                                                                                      Biochemistry 14:1842-1847(1975)
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                    REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C -> R (IN FIH; LEADS TO INEFFICIENT PROCESSING OF THE PRECURSOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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N -> D (IN REF. 5).
849015736A6E5597 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                                                                                                                                                                                                                              PARATHYROID HORMONE.
                                                                                                                                                                                                                                              Pfam; PF01279; Parathyroid; 1.
PROSITE; PS00335; PARATHYROID; 1.
Hormone; Signal; Disease mutation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 4.26
1; Mismatches
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 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF
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01-0CT-2000 (Rel. 40, Last seq
01-0CT-2000 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                         12861 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                       EMBL; J00301; AAA60215.1; -.
EMBL; V00597; CAA23843.1; -.
EMBL; A29146; CAA01956.1; -.
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115
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1BWX; 14-JAN-00.
1HPY; 14-JAN-00.
                                                                                    1HPH; 10-JUL-95.
1HTH; 15-OCT-97.
                                                                                                                                               1ZWE; 12-MAR-97
1ZWF; 16-JUN-97
                                                                                                                                                                                                                                     InterPro; IPR001415;
                                                                                                            12WA; 12-MAR-97
                                                                                                                                     12WD; 12-MAR-97
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                                                            A01536; PTHU.
A19339; A19339
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115 AA;
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32
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J. Sci. Res. Ch
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Q9XT35;
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PTH_MACFA
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Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
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MEDLINE=71076162; PubMed=5531031;
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115 PAF
12852 MW; 9
Pfam; PF01279; Parathyroid; 1. PROSITE; PS00335; PARATHYROID;
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91.2%;
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                                 Hormone; Signal
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P01268;
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Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
Potts J.T. Jr.,
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MEDLINE=76018954; PubMed=1164500;
Chu L.L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
"Porcine proparathyroid hormone. Identification, biosynthesis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Cohn D.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutharia; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The amino acid sequence of porcine parathyroid hormone.";
Biochemistry 13:1994-1999(1974).
-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BONE AND PREVENTING THEIR RENAL EXCRETION.
SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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MEDLINE=87316938; PubMed=3628009;
Schmelzer H.-J., Gross G., Widera G., Mayer H.;
Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
                                                                                                                                          PARATHYROID HORMONE.
8C2500EF24BE5597 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
                                                                                                        BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                          InterPro; IPR001415; -. Pfam; PF01279; Parathyroid; 1. PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      partial amino acid sequence.";
Biochemistry 14:3631-3635(1975).
                                                                                                           25 B3
31 B3
115 P2
12890 MW;
              EMBL; AF130257; AAD42777.1;
HSSP; P01270; 1HPY.
                                                                                                                                                                                                                        Local Similarity 97.1
nes 33; Conservative
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InterPro; IPR001415;
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PIR; B26806; B26806.
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32 1
115 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
                                                                                            Hormone; Signal
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                           Query Match
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                                                                                                                           PROPEP
                                                                                                            SIGNAL
                                                                                                                                            CHAIN
                                                                                                                                                                                                                                        Matches
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SEQUENCE FROM N.A.
MEDILINE-8005617; Pubmed-388425;
Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
Potts J.T. Jr., Rich A.;
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at the 5' terminus of the sense strand of bovine parathyroid hormone cDNA,";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-83105964; Pubmed-6185374;
Weaver C.A., Gordon D.F., Kemper B.;
"Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
Mol. Cell. Endocrinol. 28:411-424(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
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Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The N-terminal amino-acid sequence of bovine proparathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-82037785; PubMed-6170060;
Weaver C.A., Gordon D.F., Kemper B.;
"Introduction by molecular cloning of artifactual inverted
                                                                                                                              Score 168; DB 1; Length 115;
Pred. No. 4.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and nucleotide sequence of DNA coding for bovine preproparathyroid hormone."; Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
                                                                                                                                                                                                Indels
                            9FE8BCDE614BAC16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-M2Y-2000 (Rel. 39, Last annotation update)
PARATHYROLD HORMONE PRECURSOR (PARATHYRIN) (PTH).
PARATHYROID HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                   34
                                                                                                                                                                                                                                                                   1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF
                                                                                                                                                                                                                                                                                                         32 SVSEIQLMHNLGKHLSSLERVEWLRKKLQDVHNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                  TISSUE=Parathyroid;
MEDLINE=95369696; PubMed=7642102;
ROSOI T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
BOWILLS J., Capen C.C.;
"Sequences of the cDNAs encoding canine parathyroid hormone-related protein and parathyroid hormone.";
Gene 160:241 243(1995).
-:- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
-:- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SCHWELZER H.-J., Gross G., Widera G., Mayer H.;
"Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone from pig and rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FC38F77F1C8CFE56 CRC64;
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PARATHYROID HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.9%; Score 167; DB 1; L
ilarity 91.2%; Pred. No. 6.1e-15;
Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTHY_RAT STANDARD; PRT; 115 AA. P04089; Q63473; 01-NOV-1986 (Rel. 03, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=84135846; PubMed=6321505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001415; -. Pfam; PF01279; Parathyroid; 1. PROSITE; PS00335; PARATHYROID; 1.
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26 31 BY
32 115 PA
115 AA; 12957 MW;
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    Canis familiaris (Dog)
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nes 31; Conser
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                                                                                                                  SEQUENCE FROM N.A.
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                                                                         NCBI_TaxID=9615;
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Best Local 5
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                                                                                                                                                                                                                                                                 Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R., Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D., "Synthesis of a biologically active N-terminal tetratriacontapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 267:213-220(2000).
-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
-!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20090619; PubMed=10623601;
Marx U.C., Adermann R., Bayer P., Forssmann W.-G., Rosch P.;
Solution structures of human parathyroid hormone fragments
hPH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
bPHH(1-37).";
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                         "The amino acid sequence of bovine parathyroid hormone I.";
Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
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V -> G (IN REF. 4).
2ED246B348880710 CRC64;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
PTH.
                                                                                                        MEDLINE=71063634; PubMed=5275384;
Brewer H.B. Jr., Ronan R.;
"Bovine parathyroid hormone: amino acid sequence
Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.9%; Score 167; DB 1;
91.2%; Pred. No. 6.1e-15;
iive 2; Mismatches 1
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Aurbach G.D., Potts J.T. Jr.; "The amino acid sequence of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Pfam; PF01279; Parathyroid; 1.
PROSITE; PS00335; PARATHYROID; 1.
Hormone; Signal; 3D-structure.
                                                                                                                                                                                                                                                 MEDLINE=71091588; PubMed=4322265;
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                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR OF 32-68.
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nes 31; Conservative
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                                                                                                                                                                                                                                                                                                                                    parathyroid hormone."
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32
106
115 AA;
                                                                                           SEQUENCE OF 32-115.
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SIGNAL PROPEP

PTHY_CANFA

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Matches

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Gaps

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Indels

34 65

Length 115;

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STRAIN-MSB8 / DSM 3109;

MEDLINE-99287316; PubMed-10360571;

MEDLINE-99287316; PubMed-10360571;

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                           "Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.";
J. Bone Miner. Res. 3:689-698(1988).
-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN BONE AND PREVENTING THEIR RENAL EXCRETION.
-!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS)
SEQUENCE FROM N.A.
MEDIINE-89219100; Pubmed=2710135;
Russell J., Sherwood L.M.;
"Nucleotide sequence of the DNA complementary to avian (chicken)
preproparathyroid hormone mRNA and the deduced sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 121; DB 1; Length 119;
Pred. No. 5.3e-09;
9; Mismatches 3; Indels
                                                                                                                                                                                                           Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
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B309D8E772997F6E CRC64;
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Racteria: Thermotogales; Thermotoga.
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                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-89284968; PubMed=3251402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001415; -. Pfam; PF01279; Parathyroid; 1. PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                         Mol. Endocrinol. 3:325-331(1989)
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26 31
32 119 PAF
119 AA; 13943 MW; E
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30-MAY-2000 (Rel. 39, Last sequ
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63.68;
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Best Local Similarity bo...
Loca 21; Conservative
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HSSP; P01270; 12WA.
                                                                                                         precursor
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                                                                                                                                                                                                                            Kronenberg H.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hormone; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEUS OR TM0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYL_THEMA
Q9WY15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                          TISSUE=Parathyroid;
Schmelzer H.J., Gross G., Mayer H.;
"Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
                                                                                                                                                                                                                                                                                   ribonucleic acid.";
Endocrinology 136:5600-5607(1995).
-!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
-!- TISSUE SPECIFICITY: HYPOTHALANUS AND PARATHYROLD GLAND.
-!- SIMILARITY: BELONGS TO THE PARATHYROLD HORMONE FAMILY.
                                                                                                                                                                            SEQUENCE OF 32-115 FROM N.A.
STRAIN-SPRAGUE-DAMLEY: TISSUE-Brain, Parathyroid, and Liver;
MEDLINE-96079910; PubMed-7588314;
Nutley M.T., Parini S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.8%; Score 158; DB 1; Length 115; 85.3%; Pred. No. 8.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C -> Y (IN REF. 3).
A -> T (IN REF. 3).
V -> I (IN REF. 3).
V -> G (IN REF. 3).
V -> G (IN REF. 3).
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01-APR-1990 (Rel. 14, Last sequence update)
01-UL-1998 (Rel. 36, Last annotation update)
PARATHYROID HORMONE PRECURSOR (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 AA
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                                                                                                                                            Adv. Gene Technol. 21:228-229(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K01268; AAA41979.1; -.
EMBL; X05721; CAA29192.1; -.
EMBL; M54875; AAA57156.1; -.
EMBL; S080127; -; NOT_ANNOTATED_CDS.
PIR; A05091; A05091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01270; 12WB.
InterPro; IPR001415; -.
Pfam: PF01279; Parathyroid; 1.
PROSITE; PS00335; PARATHYROID; 1.
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                                       SEQUENCE OF 10-115 FROM N.A.
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"...hes 29; Conservative
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115 AA;
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P15743;
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SIGNAL PROPEP CHAIN

Gallus.

RESULT 7 PTHY_CHICK

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EMBL; M60056; AAA63639.1; JOINED
                                            PIR; JN0103; JN0103.
MGD; MGI:97800; Pthlh.
InterPro; IPR001415; -
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01-OCT-1996
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; IMALDO,
Interpro; IPR002300; -.
Interpro; IPR002302; -.
Pfam; PF00133; tRNA-synt_1; 1.
PRINTS; PR00985; TRNASYNTHLED.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aninoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
Aninoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                    SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PLAYS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91065532; PubMed=2249778;
Mangin M., Ikeda K., Broadus A.E.;
"Structure of the mouse gene encoding parathyroid hormone-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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01-AUG-1991 (Rel. 19, Last sequence update)
01-CTT-2000 (Rel. 40, Last annotation update)
PARATHYROLD HORMONE-RELATED PROTEIN PRECURSOR (PTH-RP) (PLP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.7%; Score 61; DB 1; Length 824; 37.0%; Pred. No. 2.2; 1ve 12; Mismatches 5; Indels
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genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
-!- CATALYTIC ACTIVITY: ATP + L-LEUCINE + TRNA(LEU) = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "KMSKS" REGION.
ATP (BY SIMILARITY).
7CB0252A76A844EC CRC64;
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                                                                                                      PYROPHOSPHATE + L-LEUCYL-TRNA(LEU).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::::::| ::|||:::|| | | | |:::
692 MELVNHLSQYLNSVPQEEWNRKLLREI 718
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EMBL; M60058; AAA63639.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001702; AAD35261.1; -.
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les 10; Conserv
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P22858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A., DeWille J.W., Capen C.C.; "Sequences of the cobas encoding canine parathyroid hormone-related Gene 160:241-243(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: PLAYS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                            36
175 PARATHYROID HORMONE-RELATED PROTEIN.
20100 MW; 6D27CFCC31900B45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
PY SIMILARITY.
9PARATHYROID HORMONE-RELATED PROTEIN.
93F57235C18BA2CD CRC64;
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                                                                                                                                                                                                                                         Score 58; DB 1; Length 175;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                        12; Indels
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01-ocT-1996 (Rel. 34, Last sequence update)
01-ocT-1996 (Rel. 34, Last annotation update)
PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR (PTH-RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 AA
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9; Mismatches
                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           :|| ||:|: || : : | ::| 37 AVSEHQLLHDKGKSIQDLRRRFFLHHLIAEIH 68
                                                                                                                                                                                                                                                                                                                                                              1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32
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                                                                                     POTENTIAL.
Pfam; PF01279; Parathyroid; 1.
PROSITE; PS00335; PARATHYROID; 1.
Calcium; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterFro; LPWOU1415; -.
PERM; PFF01279; Parathyroid; 1.
PROSITE; PS00335; PARATHYROID; 1.
Calcium; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Anal sac;
MEDLINE-95369696; PubMed-7642102;
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1 Similarity 34.4%;
11; Conservative
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity 34.44
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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176
176
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  Rosch P.;
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MEDLINE-8826296; PubMed=3290897;
Thiede M.A., Strewler G.J., Nissenson R.A., Rosenblatt M., Rodan G.A.;
"Human renal carcinoma expresses two messages encoding a parathyroid hormone-like peptide: evidence for the alternative splicing of a
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=88124889; PubMed=2829195;
Mangin M., Webb A.C., Dreyer B.E., Posillico J.T., Ikeda K.,
Weir E.C., Stewart A.F., Bander N.H., Milstone L., Barton D.E.,
Francke U., Broadus A.E.,
"Identification of a cDNA encoding a parathyroid hormone-like peptide
from a human tumor associated with humoral hypercalcemia of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99158054; PubMed=10050767;
Weidler M., Marx U.C., Seidel G., Schafer W., Hoffmann E., Esswein A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-89214227; PubMed-2708388; Yasuda T., Banville D., Hendy G.N., Goltzman D.; Characterization of the human parathyroid hormone-like peptide gene. Functional and evolutionary aspects."; J. Biol. Chem. 264:7720-7725(1989).
                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87260926; PubMed=2885845; Mostley J.M., Kubota M., Diefenbach-Jagger H., Wettenhall R.E.H., Kembeley J.M., Kubota M., Diefenbach-Jagger H., Wettenhall R.E.H., Kemp B.E., Suva L.J., Rodda C.P., Ebeling P.R., Hudson P.J., Zajac J.D., Martin T.J., Roda P.D., Martin T.J., Parathyroid hormone-related protein purified from a human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89306685, PubMed=2744490,
Suva L.J., Mather K.A., Gillespie M.T., Webb G.C., Ng K.W.,
Winslow G.A., Mood W.I., Martin T.J., Hudson P.J.;
Structure of the 5' flanking region of the gene encoding human
parathyrold-hormone related protein (PTHIP).";
                                                                                                                                                                                                                                                        Suva L.J., Winslow G.A., Wettenhall R.E.H., Hammonds R.G., Moseley J.M., Diefenbach-Jagger H., Rodda C.P., Kemp B.E., Rodriguez H., Chen E.Y., Hudson P.J., Martin T.J., Wood W.I.; A parathyroid hormone-related protein implicated in malignant hypercalcemia: cloning and expression.";
                                                                                                    01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR (PTH-RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer cell line.";
Proc. Natl. Acad. Sci. U.S.A. 84:5048-5052(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single-copy gene.";
Proc. Natl. Acad. Sci. U.S.A. 85:4605-4609(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 85:597-601(1988)
                                                                            177 AA
                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
:||| ||:|: || : : | : :|
AVSEHQLLHDKGKSIQDLRRRFFLHHLIAEIH 68
                                                                           PRT;
                                                                                                                                                                                                                                                  MEDLINE=87292119; PubMed=3616618;
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                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 77:95-105(1989).
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                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                        PTHLH OR PTHRP.
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                                                                            PTHR_HUMAN
P12272;
                                                  RESULT 11
PTHR_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARATHYROID HORMONE-RELATED PROTEIN.
MISSING (IN ISOFORM 2).
H -> TALLMGLKKKRINNRTHHMQLMISLFKSPLLLL
(IN ISOFORM 3).
449FDFEE954C51DB CRC64;
"The structure of human parathyroid hormone-related protein(1-34) in near-physiological solution."; FEBS Lett. 444:239-244(1999).
-!- FUNCTION: PLAYS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS A HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                         3; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DISEASE: PRODUCED BY MANY TUMORS FROM PATIENTS WITH HHM (HUMORAL HYPERCALCEMIA OF MALIGNANCY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                         -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; 1 (SHOWN HERE), 2 AND
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PROSITE; PS00335; PARATHYROID; 1.
Calcium; Hormone; Signal; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR (PTH-RP) (PLP).
                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 58; DB 1; Length 177;
Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
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EMBL; M24349; AAA60358.1; JOINED.
EMBL; M24350; AAA60359.1; JOINED.
EMBL; M24350; AAA60359.1; JOINED.
EMBL; M24349; AAA60359.1; JOINED.
EMBL; M24351; AAA60359.1; JOINED.
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EMBL; M24349; AAA60360.1; JOINED.
EMBL; J03802; AAA60218.1; -
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01-JAN-1990 (Rel. 13, Last seq
01-OCT-2000 (Rel. 40, Last anno
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34.4%;
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Best Local Similarity 34.4'
Matches 11; Conservative
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177
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MIM; 168470; -.
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or send an email to license@isb-sib.ch).
                  SEQUENCE FROM N.A.
STRAIN=ATCC 49503 / 60190;
MEDLINE=97284485; PubMed=9139899;
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59 KAINKLSQIEWFKKSVRDIRAF 80
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31.8%;
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39
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nes 7; Conser
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                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                         Venter J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=90258937; PubMed=2342478;
Karaplis A.C., Yasuda T., Hendy G.N., Goltzman D., Banville D.;
"Gene-encoding parathyroid hormone-like peptide: nucleotide sequence of the rat gene and comparison with the human homologue.";
Mol. Endocrinol. 4:441-446(1990).
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                                Thiede M.A., Rodan G.A.;
"Expression of a calcium-mobilizing parathyroid hormone-like peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: PLAYS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
NCBI_TaxID=210;
                                                                                                                              MEDLINE-89313794; PubMed-2747658; Yasuda T., Banville D., Rabbani S.A., Hendy G.N., Goltzman D.; Kat parathyroid hormone-like peptide: comparison with the human homologue and expression in malignant and normal tissue."; Mol. Endocrinol. 3:518-525(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 PARATHYROID HORMONE-RELATED PROTEIN 20204 MW; 11091EC48CA73B20 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
VIRULENCE-ASSOCIATED PROTEIN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||| ||:|: || : : | :| 37 AVSEHQLLHDKGKSIQDLRRRFFLHHLIAEIH 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01279; Parathyroid; 1.
PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M34112; AAA41889.1; -.
EMBL; M34108; AAA41889.1; JOINED.
EMBL; M34111; AAA41889.1; JOINED.
SEQUENCE FROM N.A.
MEDLINE-89019361; PubMed-3175653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ئ</u>
                                                                 in lactating mammary tissue.";
Science 242:278-280(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M21967; AAA41981.1; -. EMBL; M31603; AAA41980.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Conservative
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PIR; A34944; A34944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A34723; A34723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 AA;
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                                                                                                              SEQUENCE FROM N.A.
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005728;
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Best Local 9
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PROPEP SIGNAL CHAIN

Matches

RESULT 13

OC OC OE DIT

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                                                                                                                                                                                                                                                                                                                                                               B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                         MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.
Relson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
McKenney K., Gocayne J.D., Utterback T.W., Peterson J.D., Kelley J.M.,
Cotton M.D., Weldman J.M., Fulli C., Bowman C., Watthey L., Wallin Flayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of the gastric pathogen Helicobacter
Cao P., Cover T.L.; "High-level genetic diversity in the vapD chromosomal region of Hellcobacter pylori"; ". J. Bacteriol. 179:2852-2856(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pylori.";
Nature 388:339-547(1997).
-! MISCELLANEOUS: THERE IS NO ORTHOLOG FOR VAPD IN STRAIN J99.
-! SIMILARITY: BELONGS TO THE VAPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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MEDLINE-90272438; Pubmed-2349111;
Thiede M.A., Rutledge S.J.;
"Nucleotide sequence of a parathyroid hormone-related peptide expressed by the 10 day chicken embryo.";
Nucleic Acids Res. 18:3062-3062(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1990 (Rel. 15, Last sannotation update)
PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR (PTH-RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G -> K (IN REF. 1).
W -> N (IN REF. 1).
2475C5EBDF6F8FBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 1;
Pred. No. 1.3;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AA
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PRINTS; PR00619; GATAZNFINGER
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                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
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Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBMCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SIMILARITY: BELONGS TO THE GATA-TYPE TRANSCRIPTION FACTOR FAMILY.
FUNCTION: PLAYS A PHYSIOLOGICAL ROLE IN LACTATION, POSSIBLY AS'A HORMONE FOR THE MOBILIZATION AND/OR TRANSFER OF CALCIUM TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARATHYROID HORMONE-RELATED PROTEIN 60C8AB30ACF5293B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                       SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.7%; Score 54; DB 1; Length 176; 34.4%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Hoe K.-L., Park S.-K., Yoo O.-J.J., Yoo H.-S.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 35, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 AVSEHQLLHDKGKSIQDLRRRIFLQNLIEGVN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01279; Parathyroid; 1.
PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20226 MW;
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X52131; CAA36376.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L29051; AAB38022.1; -. EMBL; Z68887; CAA93113.1; -. HSSP; P17429; 5GAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 34.4 Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAF2 PROTEIN (GAF-2).
GAF2 OR SPAC23E2.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S10202; S10202
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01-FEB-1996
01-NOV-1997
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Q10134;
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GAF2_SCHPO
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Gaps
PROSITE; PS00344; GATA_ZN_FINGER_1; 2.
PROSITE; PS50114; GATA_ZN_FINGER_2; 2.
Transcription regulation; DNA-binding; Zinc-finger; Nuclear protein. 2N_FING 12 36 GATA-TYPE (BY SIMILARITY).
ZN_FING 172 196 GATA-TYPE (BY SIMILARITY).
CONFLICT 182 182 L -> K (IN REF. 1).
SEQUENCE 564 AA; 60611 MW; 0ED74CE0B6E210B7 CRC64;
                                                                                                                                                                                                                           5,
                                                                                                                                                                                    Length 564;
                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                  core 54; DB 1;
red. No. 12;
Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                      8, 2001, 16:30:41
                                                                                                                                                                                    Score Pred.
                                                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                                                                      537
                                                                                                                                                                                                                                                                25
                                                                                                                                                                                  30.7%;
                                                                                                                                                                                                                                                              5 IOLMHNLGKHLNSMERVEWLR
                                                                                                                                                                                                                                                                                       || :||| :|: |||| 519 IQELHNLNQHIQQID--EWLR
                                                                                                                                                                                  Query Match 30.7
Best Local Similarity 47.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Search completed: August
Job time: 84 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

August 8, 2001, 16:29:17 ; Search time 21.09 Seconds (without alignments) 213.294 Million cell updates/sec Run on:

Title: Perfect score:

US-09-447-800-1 176 1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34 Sequence:

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

425026 Total number of hits satisfying chosen parameters:

425026 segs, 132305027 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_16:* Database :

sp_archea:* sp_bacteria:*

sp_rodent:*
sp_unclassified:* sp_fungi:*
sp_human:*
sp_invertebrate:* sp_vertebrate: sp_organelle:* sp_phage:* sp_plant:* sp_mamma1:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*

SUMMARIES

	Description	Q9n1v0 equus cabal	099167 felis silve	Q9z016 mus musculu	Q9i8e9 fugu rubrip	Q9i8u2 sparus aura	Q9gk30 ovis aries	Q9glc7 oryctolagus	Q9yd49 aeropyrum p	Q15993 homo sapien	Q15992 homo sapien	Q15991 homo sapien	070327 mesocricetu	Q9v5m8 drosophila	Q9via4 drosophila	Q24164 drosophila	Q9nbk6 drosophila	Q9vcx5 drosophila	Q99786 homo sapien	Q90707 gallus gall
		S. S		,																
	ΩI	Q9N1V0	Q9GL67	970Z60	Q918E9	091802	Q9GK30	O9GLC7	Q9YD49	015993	015992	015991	070327	Q9V5M8	Q9VIA4	024164	Q9NBK6	09VCX5	099786	090707
	BB	9	9	11	13	13	9	9	-	4	4	4	11	Ŋ	Ŋ	Ŋ	Ŋ	വ	4	13
	Match Length DB	98	115	115	163	162	121	177	115	851	866	920	130	787	303	711	785	787	153	487
* Ouery	Match	7.76	6.06	88.6	44.3	42.6	33.0	33.0	31.8	30.7	30.7	30.7	30.4	30.1	29.8	29.8	29.8	29.2	29.3	29.3
	Score	172	160	156	78	75	28	58	26	54	54	54	53.5	53	52.5	- 52.5	52.5	52	51.5	51.5
Result	No.	-	7	3	₹*	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19

088447 mus musculu P88828 influenza a P88834 influenza a Q9n8v3 trypanosoma O9h3r1 homo sapien	Ogeqw8 mus musculu O95803 homo sapien O9eqh7 mus musculu		Q9u0h9 plasmodium O61199 caenorhabdi O9vlq8 drosophila		Q9nw78 homo sapien Q9h4v2 homo sapien Q9n341 caenorhabdi	O9ycm6 aeropyrum p O9erd6 mus musculu Q9ps76 gallus gall Q9ps77 gallus gall Q17633 caenorhabdi Q42396 arabidopsis
11 088447 14 P88628 14 P88834 5 Q9N8V3 4 09H3R1	11 09EQW8 4 095803 11 09EQH7	4 Q9UP21 2 Q9K7V5 3 P79004	5 Q9U0H9 5 O61199 5 O9VLO8	5 077384 2 09RQR1 4 09H4V3	4 Q9NW78 4 Q9H4V2 5 Q9N341	1 Q9YCM6 11 Q9ERD6 13 Q9PS76 13 Q9PS77 5 Q17633 10 Q42396
541 548 548 651 872	873 873 873	876 336 386	977 1038 1500	3394 96 180	279 415 561	570 590 264 292 339 490
229.3 200.3 200.3	2000	29.3 29.0	29.0 29.0	28.7 28.4 28.4	28.4	288.2 288.1 288.1 288.1 1.1 288.1
51.5 51.5 51.5 51.5	51.5 51.5 51.5	51.5 51 51	51 51	50.5 50 50	200	50 449.5 49.5 49.5
20 22 23 24	25 27 27	30 30 30	31 32 33	34 35 36	37 38 39	40 422 444 45

ALIGNMENTS

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Gaps
                                                                                                                                                                                                                       MEDLINE=20082971; PubMed=10613847;
Cactano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
Bowling A.T., Murray J.D.;
"A comparative gene map of the horse (Equus caballus).";
Genome Res. 9:1239-1249(1999).
EMBL; AF134233; AAF62247.1; -.
InterPro; IPR001415; -.
Pfam; PF01279; Parathyroid; 1.
PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                           Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                               NON_TER 1 1 SEQUENCE 86 AA; 9805 MW; 253184EA681A2022 CRC64;
                                                                         (TrEMBLrel. 15, Last sequence update) (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.7%; Score 172; DB 6; Best Local Similarity 94.1%; Pred. No. 9.6e-15; Matches 32; Conservative 2; Mismatches 0.
                             86 AA
                                                         (TrEMBLrel. 15, Created)
                             PRT;
                                                                                                     PARATHYROID HORMONE (FRAGMENT).
                             PRELIMINARY;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                        01-OCT-2000 (
01-OCT-2000 (
01-MAR-2001 (
                          Q9N1V0
Q9N1V0;
RESULT
               Q9N1V0
                               ò
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3 SVSEIQLMHNLGKHLNSVERVEWLRKKLQDVHNF 36 1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34 a

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PRELIMINARY; Q9GL67 RESULT Q9GL67 ID Q90 AC Q90 DT 01

7

115 AA. Q9GL67; 01-MAR-2001 (TrEMBLrel. 16, Created)

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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=KIDNEY
                                                   01-0CT-2000
01-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
                                      0918E9
                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
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                                                                                                                                                                                                                                                                                                                                                               Gaps
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Karaplis A.C., He B., Hiou-Tim F.F.T., Al-Akad B., Kronenberg H.M.;

"Cloning of the murine gene encoding parathyroid hormone: genomic organization and nucleotide sequence.";

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AF066075; AAC99656.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                               Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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                                                                                                                                            SEQUENCE FROM N.A.
TOTIBLO R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.,
"Molecular cloning of feline preproparathyroid hormone.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF309967; AAG30545.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.6%; Score 156; DB 11; Length 115; 82.4%; Pred. No. 1.4e-12;
                                                                                                                                                                                                                                                                                                                             Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                             POTENTIAL.
PARATHYROID HORMONE.
80CD557CC6A1A47E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
PARATHYROID HORMONE.
DA43FABBCB4E2FD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                             90.9%; Score 160; DB 6;
85.3%; Pred. No. 4.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                             32 SVSEIQFWHULGKHLSSVERVEWLRRKLQDVHNF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNF 34
                                   PREPROPARATHYROID HORMONE PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD010687; -; 1.
PROSITE; PS00335; PARATHYROID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 PC
115 P2
12825 MW;
                                                                                                                                                                                                                                                                              12921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01279; Parathyroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARATHYROID HORMONE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 85.3
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 82.4
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001415; -. InterPro; IPR003625; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00087; PTH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
32
115 AA;
                                                                                                                                                                                                                                               SIĞNAL 1
CHAIN 32
SEQUENCE 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01270; 1ZWB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD010687
                                                                                                              NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (
01-MAY-1999 (
01-MAR-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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SIGNAL
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RESULT

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Gaps
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Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Percoidei,
Sparidae, Sparus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Flanagan J.A., Power D.M., Bendell L.A., Guerreiro P.M., Fuentes J., Clark M.S., Canario A.V.M., Danks J.A., Brown B.L., Ingleton P.M.; "Cloning of the cDNA for sea bream (Sparus aurata) Parathyroid hormone-related protein."
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20314478; PubMed-10854780;
Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
Elgar G., Clark M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic structure and expression of parathyroid hormone-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.3%; Score 78; DB 13; Length 163; 46.9%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 162;
                                                                                                                                                               Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfan; PF01279; Parathyroid; 1.
ProDom; PD000206; 7; 1.
SEQUENCE 162 AA; 18722 MW; 6E8D5E07F9E5EDC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 POTENTIAL.
18698 MW; 3AC5F2C764732278 CRC64;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PARATHEROID HORMONE-RELATED PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 75; DB 13
Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gen. Comp. Endocrinol. 118:373-382(2000).
EMBL; AF197904; AAF79073.1; -. Interpro: IPRO01415; -. Interpro: IPRO03571; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|| ||||:||
38 SVSHAQLMHDKGRSLQEFRRRWLHKLLEEVH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein in a teleost, Fugu rubripes.";
Gene 250:67-79(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sparus aurata (Gilthead sea bream).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ249391; CAB94712.1; -.
InterPro; IPR001415; -.
Pfam; PF01279; Parathyroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.6%;
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Best Local Similarity
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Conservative

Matches

Q9GK30

9

RESULT Q9GK30

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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93205410; PubMed-8455946;
Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
Alternative splicing of the RBP1 gene clusters in an internal exon that encodes potential phosphorylation sites.";
Oncogene 8:949-957(1993).
EMBL: S57162; AAR25835.1; -
InterPro; IPR001606; -
Pfam; PF01388; ARID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                 Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NoV-1996 (TrEMBLrel. 01, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAN-2001 (TrEMBLrel. 16, Last annotation update)
RETINOBLASTOMA BINDING PROTEIN 1 ISOFORM III (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5724300A7032931B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l protein.
115 AA; 12603 MW; D9A02D3E1D5CC232 CRC64;
                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB 1;
Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 4;
Pred. No. 94;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  851
                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Last annot
HYPOTHETICAL 12.6 KDA PROTEIN APE1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|: ::| || || || || || ::|
17 EVAALYILHRLGPTLNYGEAVEILRERL 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 XVSEIOLMHNLGKHLNSMERVEWLRKKL 28
                                                                                         Created)
                                                     PRT;
                                                                                                                                                                                                                                                                                                           MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP000060; BAA80048.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.8%;
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38.1%;
                                                                                                        (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                   Aeropyrum.
NCBI_TaxID=56636;
                                                                                                                                                                                Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                  Q9YD49,
Q9YD49;
01-NOV-1999 (
                                                                                                        01-NOV-1999
01-MAR-2001
                                                                                                                                                                                                                                                                                          STRAIN=K1
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                  RESULT
Q9YD49
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                                                                                                                                                                                                                                                                                                                                                                                                                 Hastie P.M., Beck N.F.G.; "Expression of mRNA encoding parathyroid hormone-related peptide (PTH-rP) in ovine ovarian follicles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
 Gaps
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                                                                                                                                                                                                                                                                    Ovis aries (Sheep).
Bukaryota: Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Sukaryota: Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
ö
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McCaughern-Carucci J.F., Mitnick M., Emanuel J.R., Dworetzky ?
"Cloning and expression of rabbit parathyroid hormone-related protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58; DB 6; Length 121;
Pred. No. 3.8;
9; Mismatches 12; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.0%; Score 58; DB 6; Length 177; Best Local Similarity 34.4%; Pred. No. 5.7; Matches 11; Conservative 9; Mismatches 12; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF300703; AAG13414.1; -
SEQUENCE 177 AA; 20005 MW; E2D9F4327657B919 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF327654; AAG48348.1; ·. 1
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AA; 13657 MW; FA9437F5A5E041E1 CRC64;
                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PARATHYROID HORMONE-RELATED PEPTIDE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
11;
                                                                                                                                                            121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 177 AA
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Mismatches
                                                     1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 XVSEIQLMHNLGKHLNSMERVEWLRKKLQDVH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :||| ||:|: || : : | :| :| 37 AVSEHQLLHDKGKSIQDLRRRFFLHHLIAEIH 68
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01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
PARATHYROID HORMONE-RELATED PROTEIN.
PTHRP.
                                                                                                                                                             PRT;
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.0%;
Best Local Similarity 34.4%;
Matches 11; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9GLC7;
01-MAR-2001
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SEQUENCE
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Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.; "Cloning of Sytian hamster (Mesocricetus auratus) cytokine cDNAs and analysis of cytokine mRNA expression in experimental visceral leishmaniasis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BERKELEY;
MEDLINE-20196006; PubMed=10731132;
MEDLINE-20196006; PubMed=10731132;
Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AMR-2001 (TrEMBLrel. 16, Last annotation update)
INTERLEUKIN-10 (FRAGMENT).
ENSOSOTICETUS autratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAFE3B5FC216B380 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09V5M8; 09V5M7; 09TY63; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
38.1%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          787 AA
                                                                                                                                                                                                                                                                                                                                                 130 AA
                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53.5;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOLA PROTEIN (BTB-IV PROTEIN DOMAIN)
LOLA OR BTBIV OR CG12052 OR CG18376.
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infect. Immun. 66:2135-2142(1998).
EMBL; AF046210; AAC40095.1; -.
HSSP; P22301; 11NR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000098; -.
Pfam: PF00726; IL10; 1.
PRNUTS; PR01294; INTRLEUKIN10.
PROSITE; PS00520; INTERLEUKIN_10;
SMART; SM00188; IL10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=SPLEEN;
MEDLINE=98234044; PubMed=9573100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 KHLNSM-ERVEWLRKKLQDVHNF 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 842 NMNSTERISFLQEKLQEIRKY 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AA; 15260 MW;
                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.4%;
47.8%;
                                                                                                    14 HLNSMERVEWLRKKLQDVHNF
                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesocricetus.
NCBI_TaxID=10036;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                     070327;
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Q9V5M8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93205410; PubMed=8455946;
Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
"Alternative splicing of the RBP1 gene clusters in an internal exon that encodes potential phosphorylation sites.";
Oncogene 8:949-957(1993).
EMBL; S57160: AAB25834.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93205410; PubMed-8455946; Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.; Alternative splicing of the RBP1 gene clusters in an internal exon that encodes potential phosphorylation sites."; Oncogene 8:949-557(1993). EMBL. 557153; AAB25833.1; -... InterPro: IPR001666: -... InterPro: IPR001666: -... Pfam; PF01388; ARID: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.7%; Score 54; DB 4; Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RETINOBLASTOMA BINDING PROTEIN 1 ISOFORM II (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              920 AA; 104589 MW; BD37B5F59009570A CRC64;
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01-NOV-1996 (TLEMBLrel. 01, Created)
01-NOV-1996 (TLEMBLrel. 01, Last sequence update)
01-NAR-2001 (TLEMBLrel. 16, Last annotation update)
RETINOBLASTOMA BINDING PROTEIN 1 ISOFORM I (FRAGMENT).
                                                                                                                                                                                                                                                                          866 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         920 AA
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                                                                                                                                                                                                                                                                          PRT;
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                                                             773 NANSTERISFLØEKLØEIRKY 793
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                         14 HLNSMERVEWLRKKLQDVHNF 34
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NON_TER 1
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SMART; SM00298; CHROMO; 1.
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                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE
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10 201591
AC 015991
AC 015991
DT 01-NOV
DT 01-NOV
DT 01-NOV
DC NEBLINO
CS HOMO S
CC ENKATY
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CC ENKATY
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Length 130; Indels Created)

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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., And K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Chandra I., Barraktaroglu L., Beatley E.M., Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., A cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., Doub L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Rolleck A., Gong F., Gorrell J.H., Gu.Z., Guan P., Harris M., Glasser K., Gorleck A., Gong F., Gorrell J.H., Gu.Z., Guan P., Harris M., Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Rak McKuluo G., Milshna N.V., Mobarty C., Morris J., Morpherson D., Mount S.M., Moy M., Murphy B., Murphy L., Wuzny D.M., Nelson D.K., Reisen D.R., Palazzolo M., Pittann G.S., Pan S., Pollard J., Puti V., Reese M.G., Shue B.C., Sidan-Klamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Sidan-Klamos I., Simpson M., Skupski M.P., Smith T., Sheng E.Y., Wassarman D.A., Weinstock G.M., Wang S., Zhu X., Smith H.O., Rangobs R.A., Myers E.W., Rubin G.M., Wonter J.C., Scheeler F., Wang S., Yao Q.A., And J., Marphy G., Dang S., Zhu X., Smith H.O., Rangobs R.A., Myers E.W., Rubin G.M., Venter J.C., Scheeler F., Sprad H. W. Rubin G.M., Venter J.C., Scheeler F., Sprad R. W., Shong K.J., Zhan M., Zhang G., Zhao Q., Zhao Q., Zhao Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Schee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95024186; PubMed-7938017; Zollman S., Godt D., Prive G.G., Couderc J.L., Laski F.A.; The BTB domain, found primarily in zinc finger proteins, defines an evolutionarily conserved family that includes several developmentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN SHORT ISOFORM).
6F20570E6C1A4702 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 5-119 FROM N.A. MEDLINE=95024186; PubMed=7938017;
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FlyBase; FBgn0005630; lola.
InterPro; IPR000210; -.
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Pfam; PF00651; BTB; 1.
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Best Local Similarity
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SEQUENCE
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REPLINE FROM N.A.

REPLINE—20196006; PubMed=10731132;

RA Adman M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adman M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogars Y.-H.C., Blazej K.G., Change M., Pfeliffer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley B.M.,

RA Ballew R.M., Basu D.A., Berman B.P., Bhandari D., Bolshakov S.,

RA Ballew R.M., Basu D.A., Butler H., Cadleu B., Center A., Chadra I.,

RA Buttis R.C., Busam D.A., Butler H., Cadleu B., Center A., Chadra I.,

RA Buttis R.C., Busam D.A., Butler H., Cadleu B., Dunkov B.C., Dunn P.,

RA Dodson R., Downes M., Dayan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson R., Downes M., Dayan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson R., Doup L.E., Downes M., Digan-Rocha S., Pleischmann W.,

RA Dodson R., Doup E.E., Gorge R.S., Gelbart W.M., Glasser R.,

RA Hostin D., Houston R.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston R.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston R.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Liu X., Mattel B., McIntosh T.C., McLeed M.P., Morris J., Mosherson D.,

RA Lasko P., Lei Y. Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei W., Mobarry C., Morris J., Morris J., Mosherson D.,

RA Lasko P., Lei W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Relazzolo M., Pittunan G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Relazzolo M., Pittunan G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shee Relazzolo M., Pittunan G.S., Pan S., Pollard J., Puri Y., Saneh H.,

RA Sheeler K., Spradling A.C., Stapleton M., Stopeler F., Shen H.,

Schredling A.C., Stapleter R., Scheler F., Shen H.,

Schredling A.C., Stapleter R., Stanen R., Wang A. H., Wang A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sylrskas R., Tector C., Trucer R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A., YeJ., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhong G., Zhu S., Zhu K., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Smith H.O., Science 287:2185-2195(2000)
                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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SEQUENCE 303 AA; 35689 MW; 57BA402F6AF764D5 CRC64;
                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 LINEEQLLQSMHRKLNNLNTIMSIYKYMEWLHRKL 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0015770; MstProx.
01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 28.6%
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                                                                                                           MSTPROX PROTEIN.
MSTPROX OR CG1149.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro:
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Q24164;
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ij

303 AA.

PRELIMINARY;

Q9VIA4 Q9VIA4;

09VIA4 ID 09

RESULT 14

Dp

us-09-447-800-1.rspt

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
DMASTPROX.
MSTPROX OR CG1149.
Drosophila melanogaster (Fruit fly).
Bridaryota; Merazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Merazoa, Arthropoda; Tracheata; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                MEDLINE—96215042; PubMed=8621445;

MEDLINE—96215042; PubMed=8621445;

MICHAM J.L., Parnet P., Bonnert T.P., Garka K.E., Gerhart M.J.,
Slack J.L., Parnet P., Bonnert T.P., Garka K.E., Gerhart M.J.,
Slack J.L., Gayle M.A., Dower S.K., Sims J.E.;
TI/ST2 signaling establishes it as a member of an expanding
interleukin.1 receptor family ";
J. Biol. Chem. 271:5777-5783(1996).

BMBL: U42425; AAC46999.1.
FlyBase; FEGN0015770; MSLProx.
RITEPPO; IPR000157; -.
FlyBase; PR000157; -.
RITEPPO; IPR000157; -.
RITEPPO; IPR00151; -.
REPPO; IPR00151; -.
REPPO; IPR00152; -.
REPPO; IPR00152; -.
REPPO; IPR00152; TIR; 1.
REPPO; IPR00255; TIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.8%; Score 52.5; DB 5; Length 711; 28.6%; Pred. No. 1.2e+02; tive 11; Mismatches 7; Indels ...
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Best Local Similarity 28.6
Matches 10; Conservative
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Search completed: August 8, 2001, 16:31:09

9 2 2 Search completed: August 8, 2001, 16:31:09 Job time: 112 séc